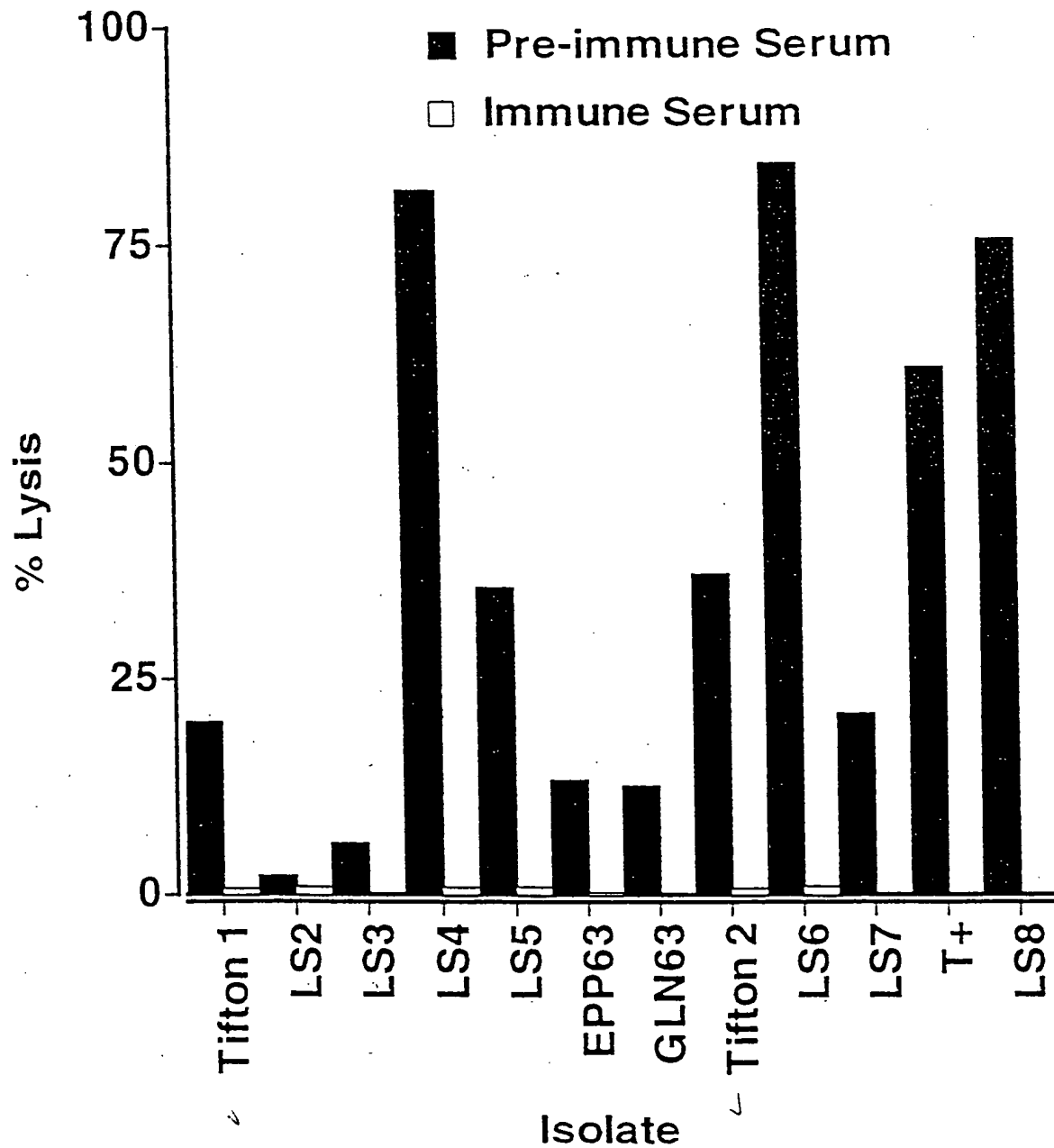
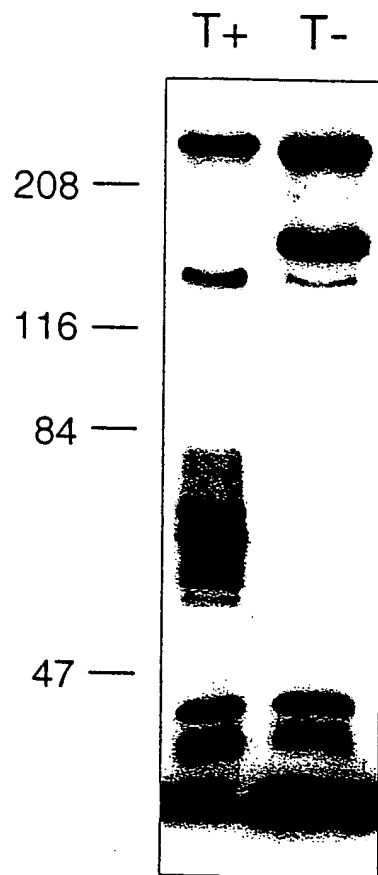


FIG. 1



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FIG. 2



## Appendix A update-July 1999

Bases 1-1200

Amino acids 1-400

1	ATGTCCAATATAAAATGTAATTAATCTAATATTCAAGCAGGCTTGAATTCAACAAAGTCT	60
1	M S N I N V I K S N I Q A G L N S T K S	20
61	GGATTAAAAAATCTTTACTTGGCTATTCCCAAAGATTATGATCCGCAAAAAGGTGGGACT	120
21	G L K N L Y L A I P K D Y D P Q K G G T	40
121	TTAAATGATTTTATTAAAGCTGCTGATGAATTAGGTATTGCTCGTTTAGCAGAAGAGCCT	180
41	L N D F I K A A D E L G I A R L A E E P	60
181	AATCACACTGAAACAGCAAAAAAATCTGTTGACACAGTAAATCAGTTTCTCTCTCACA	240
61	N H T E T A K K S V D T V N Q F L S L T	80
241	CAAACGGTATTGCTATTTCTGCAACAAAATTAGAAAAGTTCTTACAAAAACATTCTACC	300
81	Q T G I A I S A T K L E K F L Q K H S T	100
301	AATAAGTTAGCCAAAGGGTTAGACAGTGTAGAAAATATTGATCGTAAATTAGGTAAAGCA	360
101	N K L A K G L D S V E N I D R K L G K A	120
361	AGTAATGTATTATCAACATTAAGCTCTTTTTTGGGCACTGCATTAGCGGGTATAGAATT	420
121	S N V L S T L S S F L G T A L A G I E L	140
421	GATTCTTTAATCAAAAAAGGTGATGCTGCACCTGATGCTTTGGCTAAAGCTAGTATTGAC	480
141	D S L I K K G D A A P D A L A K A S I D	160
481	TTGATTAATGAGATAATTGGTAATCTATCTCAGAGTACTCAAACGATTGAAGCATTTTCT	540
161	L I N E I I G N L S Q S T Q T I E A F S	180
541	TCACAGTTAGCAAAGTTAGGTTCTACTATATCGCAGGCTAAAGGCTTCTCTAATATAGGA	600
181	S Q L A K L G S T I S Q A K G F S N I G	200
601	AACAAGTTGCAAAACTTAAATTTTTCTAAAACAAATCTTGGTTTGAAATAATTACTGGT	660
201	N K L Q N L N F S K T N L G L E I I T G	220
661	TTGCTATCAGGCATTTCTGCAGGCTTTGCTTTAGCGGATAAAAATGCATCGACTGGCAAA	720
221	L L S G I S A G F A L A D K N A S T G K	240
721	AAAGTTGCTGCAGGTTTTGAATTAAGCAATCAAGTTATTGGTAATGTAACAAAGCAATT	780
241	K V A A G F E L S N Q V I G N V T K A I	260
781	TCTTCATATGTTTTAGCACACGTGTTGCTGCTGGTCTATCACTACTGGTGCTGTTGCT	840
261	S S Y V L A Q R V A A G L S T T G A V A	280
841	GCTTTAATTACTTCATCGATTATGTTGGCAATTAGTCCTTTGGCATTATGAATGCAGCA	900
281	A L I T S S I M L A I S P L A F M N A A	300
901	GATAAATTCAATCATGCTAATGCTCTTGATGAGTTTGCAAAACAATCCGAAAATTTGGC	960
301	D K F N H A N A L D E F A K Q F R K F G	320
961	TATGATGGGGATCATTTATTGGCTGAATATCAGCGTGGTGTGGGTACTATTGAAGCTTCA	1020
321	Y D G D H L L A E Y Q R G V G T I E A S	340
1021	TTAACTACAATTAGTACGGCATTAGGTGCAGTTTCTGCTGGTGTTCGCTGCTGCTGTA	1080
341	L T T I S T A L G A V S A G V S A A A V	360
1081	GGATCTGCTGTTGGTGCACCGATTGCACTATTAGTTGCAGGTGTTACAGGATTGATCTCT	1140
361	G S A V G A P I A L L V A G V T G L I S	380
1141	GGAATTTTAGAAGCGTCTAAACAGGCAATGTTTGAAAGTGTGCTAACCGTTTACAAGGT	1200
381	G I L E A S K Q A M F E S V A N R L Q G	400

 $m \times A$ 

+

MoxA

[illegible]

Appendix A update-July 1999, continued

Bases 1201-2400  
Amino acids 401-800

1201	AAAATTTTAGAGTGGGAAAAGCAAAATGGCGGTCAGAACTATTTTGATAAAGGCTATGAT	1260
401	K I L E W E K Q N G G Q N Y F D K G Y D	420
1261	TCTCGTTATGCTGCTTATTTAGCTAATAACTTAAATTTTTGTCTGAGCTAAATAAAGAG	1320
421	S R Y A A Y L A N N L K F L S E L N K E	440
1321	TTGGAAGCTGAACGTGTTATTGCAATCACCCAACAACGTTGGGATAATAATATTGGTGAG	1380
441	L E A E R V I A I T Q Q R W D N N I G E	460
1381	TTAGCAGGTATTACCAAATTGGGTGAACGCATTAAGAGCGGAAAAGCTTATGCAGATGCT	1440
461	L A G I T K L G E R I K S G K A Y A D A	480
1441	TTTGAAGATGGCAAGAAAGTTGAAGCTGGTTCCAATATTACTTTGGATGCTAAAAGCTGGT	1500
481	F E D G K K V E A G S N I T L D A K T G	500
1501	ATCATAGACATTAGTAATTCAAATGGGAAAAAAACGCAAGCGTTGCATTTCACTTCGCCT	1560
501	I I D I S N S N G K K T Q A L H F T S P	520
1561	TTGTTAACAGCAGGAACTGAATCACGTGAACGTTTAACTAATGGTAAATACTCTTATATT	1620
521	L L T A G T E S R E R L T N G K Y S Y I	540
1621	AATAAGTTAAATTCGGACGTGTAAAAAACTGGCAAGTTACAGATGGAGAGGCTAGTTCT	1680
541	N K L K F G R V K N W Q V T D G E A S S	560
1681	AAATTAGATTTCTCTAAAGTTATTCAGCGTGTAGCCGAGACAGAAGGCACAGACGAGATT	1740
561	K L D F S K V I Q R V A E T E G T D E I	580
1741	GGTCTAATAGTAAATGCAAAAGCTGGCAATGACGATATCTTTGTTGGTCAAGGTAAAATG	1800
581	G L I V N A K A G N D D I F V G Q G K M	600
1801	AATATTGATGGTGGAGATGGACACGATCGTGTCTTCTATAGTAAAGACGGAGGATTTGGT	1860
601	N I D G G D G H D R V F Y S K D G G F G	620
1861	AATATTACTGTAGATGGTACGAGTGCAACAGAAGCAGGCAGTTATACAGTTAATCGTAAG	1920
621	N I T V D G T S A T E A G S Y T V N R K	640
1921	GTTGCTCGAGGTGATATCTACCATGAAGTTGTGAAGCGTCAAGAAACCAAGGTGGGTAAA	1980
641	V A R G D I Y H E V V K R Q E T K V G K	660
1981	CGTACTGAAACTATCCAGTATCGTGATTATGAATTAAGAAAAGTTGGGTATGGTTATCAG	2040
661	R T E T I Q Y R D Y E L R K V G Y G Y Q	680
2041	TCTACCGATAATTTGAAATCAGTAGAAGAAGTAATTGGTTCTCAATTTAATGATGTATTC	2100
681	S T D N L K S V E E V I G S Q F N D V F	700
2101	AAAGGTTCTAAATTCACGACATATTCATAGTGGTGAAGGTGATGATTTACTCGATGGT	2160
701	K G S K F N D I F H S G E G D D L L D G	720
2161	GGTGCTGGTGACGACCGCTTGTGGTGGTAAAGGCAACGATCGACTTTCTGGAGATGAA	2220
721	G A G D D R L F G G K G N D R L S G D E	740
2221	GGCGATGATTTACTCGATGGCGGTTCTGGTGATGATGTATTAATGGTGGTGCTGGTAAT	2280
741	G D D L L D G G S G D D V L N G G A G N	760
2281	GATGTCTATATCTTTCCGAAAGGTGATGGTAAATGATACTTTGTACGATGGCACGGGCAAT	2340
761	D V Y I F R K G D G N D T L Y D G T G N	780
2341	GATAAATTAGCATTTGCAGATGCAAATATATCTGATATTATGATTGAACGTACCAAAGAG	2400
781	D K L A F A D A N I S D I M I E R T K E	800

1201-2400 bases  
401-800 amino acids

Amino acids 801-927

2401	GGTATTATAGTTAAACGAAATGATCATTACAGGTAGTATTAACATACCAAGATGGTACATA	2460
801	G I I V K R N D H S G S I N I P R W Y I	820
2461	ACATCAAATTTACAAAATTATCAAAGTAATAAAACAGATCATAAAAATTGAGCAACTAATT	2520
821	T S N L Q N Y Q S N K T D H K I E Q L I	840
2521	GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTTTGCAAGATAAGAAA	2580
841	G K D G S Y I T S D Q I D K I L Q D K K	860
2581	GATGGTACAGTAATTACATCTCAAGAATTGAAAAAGCTTGCTGATGAGAATAAGAGCCAA	2640
861	D G T V I T S Q E L K K L A D E N K S Q	880
2641	AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGGTCAATGGCACTA	2700
881	K L S A S D I A S S L N K L V G S M A L	900
2701	TTTGGTACAGCAAATAGTGTGAGTTCTAACGCCTTACAGCCAATTACACAACCAACTCAA	2760
901	F G T A N S V S S N A L Q P I T Q P T Q	920
2761	GGAATTTTGGCTCCAAGTGTTTAG	2784
921	G I L A P S V *	928

MbxA	Lkta	.. - M G T R R T T S	.. N G T X N T T T A T	.. S G S G L H K K S	V I K S N I O A G L	N S T K S G L K N L	Y L A I P K . D Y	D P Q K G	38
ApxiIA	HlyA	M S K T T T A A Q L M	S S L Q S A Q K K N G	K N K L N Q A G T T	.. Q S L T O A G	S S L M T G A R M	I L Y T P Q N Q Y	D S T E R G	59
			S T L Q S Q K K S A	A N K L R S A G Q S	L K N G L T O T G	H S L Q N G A R M	I L Y T P Q N Q Y	D S T E R G	62
					T M D A L K K A A E	Q T R N A . N . L	I L T P T Q K D Y K	.. . . .	61
MbxA	Lkta	G T T W D L K A A	D E L G I A R L A E	E P N H G E T A R K	V D T V N Q F L S	L T T C G I A I S A	T K L K H P L O K H	S E N N L K	103
ApxiIA	HlyA	S G V Q D L V K A A	N L G I E V V R E	E R S N L D I A K T	S F D T T O M T L G	E T E R G I V L V A	P O L D M L L O K	.. N P R I	121
		S S N D L V . T A	D E L G I E V V Y	E N G T A I T H Q	V P G T A L K L I G	L T E R G . T I F A	P O L D M L L Q N Y	Q . . . .	125
									124
MbxA	Lkta	A K G L . D S V E N	I O R K L G K A S N	V L S T . S S F L G	T A L A G I E L D S	L I K K . . . . G D	A A P D A L A K A S	I . L I N	163
ApxiIA	HlyA	G Q A T . G S A S S	I S O B A N K R A K T	V L S G G F Q S I L G	S V L A G M D L D R	A L Q N . . . . N	S N O H A L A K A G	L E L . .	180
		G K K L . G S A S N	I G D N L O K A G S	V L S T F O N F L G	T A L S S N K L D R	L I K K Q K S G G M	V S S S E L A K A S	I S L . .	185
									189
MbxA	Lkta	E I I G N T S Q S T	O T . L A P S S Q L	A K L Q S T . S Q A	K G F S N . G N R L	Q N L . G F S K T N	L G L . I I T G L L	S G I S A	227
ApxiIA	HlyA	S L I E T A N S V	K T L D E F G G Q I	S O F G S K L Q N I	K G L G T L G D R L	K N L . N G L D K A G	L G L D . I S G L L	S G A I A	245
		E V . D T A A S S V	O T V O A F A R Q I	S K L G S H L Q N V	K H L G G L S N K L	Q N L P L O L G K A S	L G L D . I S G L L	S G A I A	250
			N N V S S F S . Q L	N K L G S V L S N T	K H L E R G V G N R L	Q N L P N L D N I G	A G L D T S S G L L	S A I S A	253
MbxA	Lkta	G P A L A D K H A S	T G K V A A G F E	L S N O V I G N V T	K A I S S Y L A Q	R V A A G L S T T G	A V A A L I T S S	M L A I S	292
ApxiIA	HlyA	A L . L A D K H A S	T A K V A A G F E	L A N O V I G N V T	K A V S S Y L A Q	R V A A G L S T T G	P V A A L I A S T V	S L A I S	310
		G L L A D K H A S	T A K V A A G F E	L A N O V I G N V T	K A V S S Y L A Q	R V A A G L S T T G	P V A A L I A S T V	A L A I S	315
		S F . L S N A A D A	T G T N A A A G V E	L T T K V . G N V G	K G I S Q T I . A Q	R A A Q G L S T S A	A A A G L I A S V M	T L A I S	318
MbxA	Lkta	P P A . L A A D H	P H A A L M E T	A K O F . H F G D	G D N H L A S Y Q R	G V G T I D A S L V	T I N T A L G A V S	A G V S A	357
ApxiIA	HlyA	P P A . L A A D H	P H A A L M E T	A K O F . H F G D	G D N H L A S Y Q R	G V G T I D A S L V	T I N T A L G A V S	A G V S A	375
		P L S . L S T A D H	P K R A N K I S E	S . R P F K L G Y D	G D S L L A F N R	E T G T I D A S L V	T I N T A L A A I S	C G V S A	380
									383
MbxA	Lkta	A A V G S A V G A P	I A L L V A G V T G	L I S G I L E A S N	Q A M F E S V A S N	L Q K K I L E W E K	N N G G Q N Y F E K	G Y D S R	422
ApxiIA	HlyA	A A V G S A V G A P	I A L L V A G V T G	L I S G I L E A S N	Q A M F E S V A S N	L Q K K I L E W E K	N N G G Q N Y F E K	G Y D S R	440
		A S T T . S L V G A P	V S A L L V A G V G	L I S G I L E A S N	Q A M F E S V A S N	V H D . I V S W E K	K H N K N Y P E K	G Y D S R	444
									447
MbxA	Lkta	Y A A Y L A N N N R	P L S L N K K E L	A E R V I A I T Q Q	R W D N N I G E L A	G I T . L G E . I K	S G K A Y A D A P E	M G K K V	487
ApxiIA	HlyA	Y L A D L O D E N K	P L S L N K K E L	A E R V I A I T Q Q	R W D N N I G E L A	G I T . L G E . I K	S G K A Y A D A P E	E G K H I	505
		H A . F L D N F R	P L S L N K K E L	A E R V I A I T Q Q	R W D N N I G E L A	G I T . L G E . I K	S G K A Y A D A P E	E G K H I	509
									512

FIG. 5

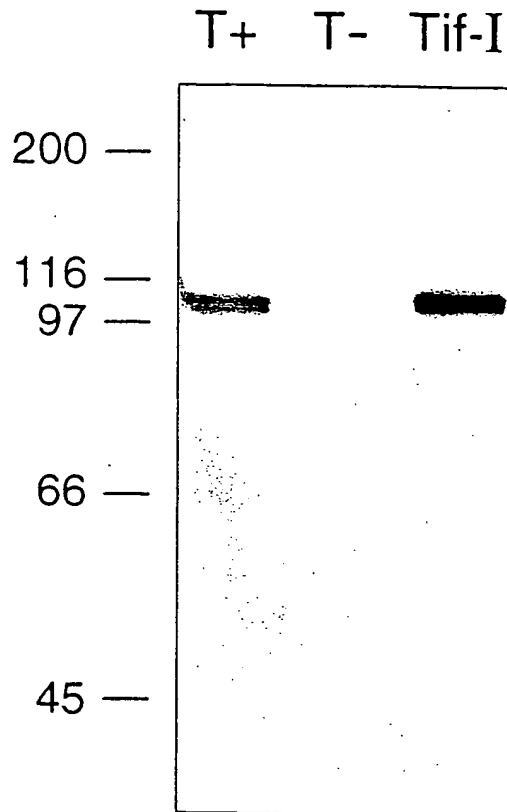
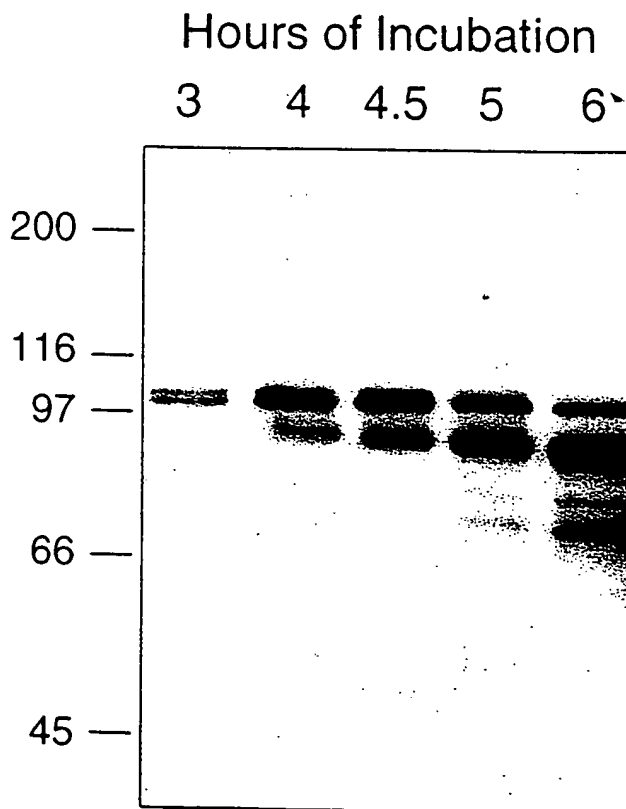
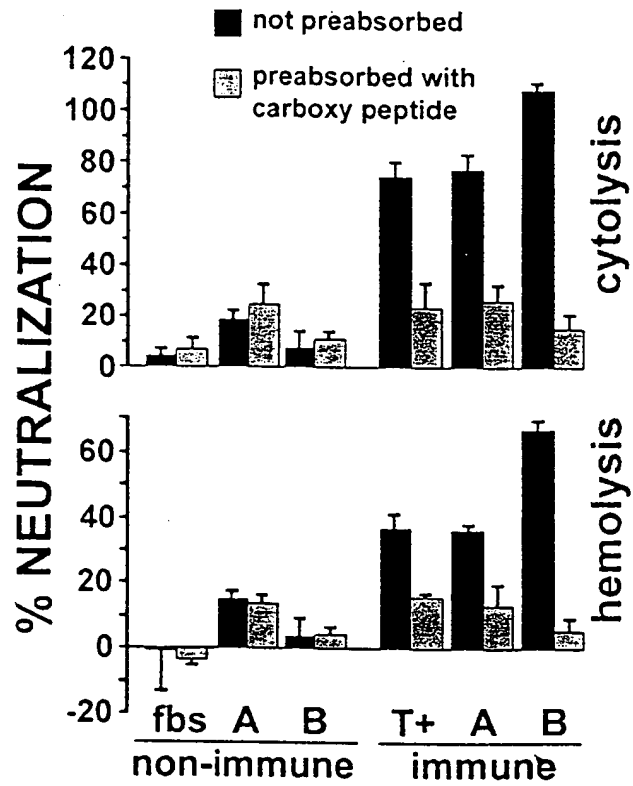


FIG. 6



# FIG. 7





1 ATGGGTGGTGATACTTCTTTAATTGACTTAATTTACAAACCCCTTAATAGTAATTTAGTT 60  
1 M G G D T S L I L N L Q T L N S N L V 20

61 ATGATAGATTATGCTCAACAACCTGCTCTATCTGCTCTGGTTATCCTTGCCAAATACTAT 120  
21 M I D Y A Q Q P A L S A L V I L A K Y Y 40

121 GGTATTTCTGCAAGTCCAGCAGACATTATGCATCAGTTTTCTGATAATACAAAAGGAGAC 180  
41 G I S A S P A D I M H Q F S D N T K G D 60

181 CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAGGTAAAGATTATA 240  
61 L N E I E W M L A A K K L E L K V K I I 80

241 AAACAGCCTTTAACTCGATTGTCAATGATAACACTTCCTGCTTTGGTGTGGTGTGATAAT 300  
81 K Q P L T R L S M I T L P A L V W C D N 100

301 AAGCCCGATTAGATCAAAATTTAACTCTCATTTTATACTAACTAAAATTGATGGGGTG 360  
101 K P D L D Q N L N S H F I L T K I D G V 120

361 GGATCTGCTGCAAAATATCTCATCTACGATTTGATTGAGAATCGTCCATAATATTAGAT 420  
121 G S A A K Y L I Y D L I E N R P I I L D 140

421 GCAAGTGAGTTTTCTGAAAGATATTCTGGTAAGTTAATGCTAGTAACTTCCCGTGC GTCA 480  
141 A S E F S E R Y S G K L M L V T S R A S 160

481 ATATTGGGTTTCATTGGCTAAATTTGATTTTACTTGGTTTATTCCTGCGGTAATCAAATAT 540  
161 I L G S L A K F D F T W F I P A V I K Y 180

541 CGTTATATTTTTTTGAAGTCATCGTTATTTTCAGTGGTGCTACAGATTTTTGCTCTGATT 600  
181 R Y I F F E V I V I S V V L Q I F A L I 200

601 ACGCCATTGTTTTTTCAGGTTGTGATGGATAAGGTATTGGTGCATCGTGGTTTTTCTACT 660  
201 T P L F F Q V V M D K V L V H R G F S T 220

661 CTGGATGTGGTAGCGATTGCCTTGTTGGTAGTAAGTTTATTTGAAGTCATTTTAAGTGGT 720  
221 L D V V A I A L L V V S L F E V I L S G 240

721 CTACGCACTTATATTTTTGCTCATACAACCTCTCGAATTGATGTAGAGCTAGGAGCACGA 780  
241 L R T Y I F A H T T S R I D V E L G A R 260

781 TTATTTTCGTCTATCTATTAGCTCTACCGCTTGCTTATTTTGAGAGTAGAAGAGTAGGCGAT 840  
261 L F R H L L A L P L A Y F E S R R V G D 280

841 ACAGTTGCACGTATACGTGAATTGGAACATATCCGCAATTTCTTAACTGGTCAAGCTCTC 900  
281 T V A R I R E L E H I R N F L T G Q A L 300

901 ACTTCAGTTTTAGATTTGGTGTTTTCTTTATATTCTTGTTTGAATGTGGTATTACAGC 960  
301 T S V L D L V F S F I F L F V M W Y Y S 320

961 CCTACTTTAACTGGTAGTTTTGGCATCATTACCAATATATGCGTTTTGGTCTGCCTTT 1020  
321 P T L T L V V L A S L P I Y A F W S A F 340

1021 ATTAGCCCAATTTTACGCACTCGACTAAATGATCAATTTGCACGCAATGCAGATAATCAA 1080  
341 I S P I L R T R L N D Q F A R N A D N Q 360

1081 TCTTTTTTAGTGAAAGTATTACTGCGGTTGGTACGGTAAAAGCAATGGCAGTTGAACCT 1140  
361 S F L V E S I T A V G T V K A M A V E P 380

1141 CAAATGACCCGTCGCTGGGATAATCAATTAGCAGCTTATGTGGTTTCTAGTTTTCGGGTA 1200  
381 Q M T R R W D N Q L A A Y V V S S F R V 400

1201 GCTAAGTTGGCAATGGTTGGGCAGCAAGGAGTACAACCTCATTCAAAAGATGGTTATTGTG 1260  
401 A K L A M V G Q Q G V Q L I Q K M V I V 420

1261 GCAACTCTATGGATTGGTGCAAAATTTGGAATTTGAAGGCAAGCTATCGGTAGGTCAATTA 1320  
421 A T L W I G A K L V I E G K L S V G Q L 440

mbx B  
mbx B

**FIG 8-1**

1321	ATAGCATTTAATATGCTGGCAGGTCAGGTGGCCGCTCCTGTTATCCGCCTGGCACAGCTA	1380
441	I A F N M L A G V A A P V I R L A Q L	460
1381	TGGCAAGATTTTCAGCAAGTAGGTATTTTCAGTGGCGAGATTGGGTGATATTTTAAATACT	1440
461	W Q D F Q Q V G I S V A R L G D I L N T	480
1441	CCAAGTGGCATTCTACATCTCGCTTAACTTTACCTGATATTAAGGGTGATATTACATTT	1500
481	P T E H S T S R L T L P D I K G D I T F	500
1501	GAAAATGTTGATTTTCGCTACAAAATAGATGGGCATTTAATATTACAGAATTTAAATTTA	1560
501	E N V D F R Y K I D G H L I L Q N L N L	520
1561	CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAGGTAAATCAACA	1620
521	Q I N A G E I L G I V G R S G S G K S T	540
1621	TTGACAAAATTAGTACAGCGTTTATATGTACCAGAAAATGGGCGAATATTAGTTGATGGA	1680
541	L T K L V Q R L Y V P E N G R I L V D G	560
1681	AACGATTTGGCATTAGCTGATCCCGCTTGGCTGCGTCGCCAAGTGGGTGTTGTTTTGCAG	1740
561	N D L A L A D P A W L R R Q V G V V L Q	580
1741	GAAAATGTGTTACTCAATCGTAGTATTCGAGATAATATTGCCCTAACTGATACGGGCATG	1800
581	E N V L L N R S I R D N I A L T D T G M	600
1801	TCATTAGAGTTTATTATCCAGGCTGCCAAGATGTCTGGGGCACATGACTTTATTATGGAA	1860
601	S L E F I I Q A A K M S G A H D F I M E	620
1861	TTGCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTGAGGTGGACAA	1920
621	L P E G Y D T I V G E Q G A G L S G G Q	640
1921	CGCCAGCGTATCGCTATTGCGCGTGCTTTAATTACCAATCCGCGTATTTTGATTTTGAT	1980
641	R Q R I A I A R A L I T N P R I L I F D	660
1981	GAAGCTACTAGTGCATTAGACTATGAGTCGGAAAGGGCTATTATGCAAAATATGCAGGCA	2040
661	E A T S A L D Y E S E R A I M Q N M Q A	680
2041	ATTTGCCAAGGTAGAACAGTGTTGATTATTGCACATCGCTTATCTACCGTAAAAATGGCA	2100
681	I C Q G R T V L I I A H R L S T V K M A	700
2101	CATCGCATTATTGCAATGGACAAGGGGAAAATTGTAGAGCAAGGCACACATCAAGAATTG	2160
701	H R I I A M D K G K I V E Q G T H Q E L	720
2161	TTGCAAAAAGAAGATGGTTACTATCGTTATTTATATGATTTGCAGAATGGATAAA	2215
721	L Q K E D G Y Y R Y L Y D L Q N G *	739

**F168-2**

SEQ ID NO: 30  
SEQ ID NO: 18

# FIG. 9

MbxB	---	MD	YAQQPALSA	LVILAKYIG	ISASPAIM	HQFSONTG	DINBIEM	AANKLEL	55
LktB	MANQRND	L....GLVA	LTMLAQYHN	ISLNPBEIK	SKFDLDGKG	LSLTAWLL	AANKSLAL	56	
ApXIB	MDFYREED	Y....GLYA	LTILAQYHN	IAVNPBEIK	SKFDLGGG	LDLTAWLL	AANKSLAL	55	
HlyB	MO SCKID	Y....GLYA	LEILAQYHN	SVNPBEIK	SKFDLGGG	LGLTAWLL	AANKSLAL	55	
MbxB	RVKIRIQP	TRLSMITLP	ALVWCNKPP	DLDQNLNSB	FILTRIDGV	GSAKYLHY	DLINRP	116	
LktB	KARHIRKRI	SRLHLNLP	ALVWQDN	.....GKB	FILTRVD	TNNRTLY	NLEQDAP	107	
ApXIB	KARQVKKRI	DRLAPIALP	ALVWRED	.....GKB	FILTRID	NSAKKLYF	DLTHBP	106	
HlyB	KVQVKKRI	DRLNPLS	ALVWRED	.....GKB	FILTRVS	KBANRTLY	DLQRNP	106	
MbxB	ILLASRPS	ERYSGRLML	VTSRASILQ	SLARPDFTW	PIPAVIRK	YIFPBYV	SVVLQIF	177	
LktB	QILSTDSBP	ACYQGLIL	VTSRASVVG	QLAKPDFTW	PIPAVIRK	RIPBTIV	SIFLOIF	168	
ApXIB	RILEQARBP	SLYQGLIL	VASRASIVG	KLAKPDFTW	PIPAVIRK	RIPBTIV	SIFLOIF	167	
HlyB	RLEQSBP	ALYQGHIL	VASRSVAG	KLAKPDFTW	PIPAVIRK	RIPBTIV	SIFLOIF	167	
MbxB	ALITPLFPQ	VVMKRVLVH	RGPSTLDV	AALLVVS	FEILSGLR	TYFABTS	RIDVELG	238	
LktB	ALITPLFPQ	VVMKRVLVH	RGPSTLNI	TVALAIV	FEIVLSGLR	TYFABTS	RIDVELG	229	
ApXIB	ALITPLFPQ	VVMKRVLVH	RGPSTLVI	TVALAIVL	FEIVLSGLR	TYFABTS	RIDVELG	228	
HlyB	ALITPLFPQ	VVMKRVLVH	RGPSTLVI	TVALSVV	FEILSGLR	TYFABTS	RIDVELG	228	
MbxB	ARLPRHLLA	LPAYPESR	RVGDTVAR	BELHIRNF	LTGOALTSV	LIVPSPIP	LVMWY	299	
LktB	AKLPRHLLS	LPISYPENR	RVGDTVARV	RELDQIRNF	LTGOALTSV	LIVPSPIP	LVMWY	290	
ApXIB	AKLPRHLLA	LPISYPENR	RVGDTVARV	RELDQIRNF	LTGOALTSV	LIVPSPIP	LVMWY	289	
HlyB	AKLPRHLLA	LPISYPESR	RVGDTVARV	RELDQIRNF	LTGOALTSV	LIVPSPIP	LVMWY	289	
MbxB	SPTLTLVL	ASLPIYAFW	SAPISPILB	TRLNDQPAR	NADNOSPLV	SSATAGH	KANAVSP	360	
LktB	SPKLTTLVL	GSLPCYILW	SIFISPILB	RRLDERFAR	SADNOSPLV	SSVTAINTI	KANAVSP	351	
ApXIB	SPKLTTLVL	GSLPCYILW	SIFISPILB	RRLDERFAR	SADNOSPLV	SSVTAINTI	KANAVSP	350	
HlyB	SPKLTTLVL	FSLPCYIAM	SIFISPILB	RRLDERFAR	NADNOSPLV	SSVTAINTI	KANAVSP	350	
MbxB	QMTRRWONQ	LAAYVVSF	RVAKLAMIG	QQGVOLIQ	MVLVATLW	GAKLVISGK	LSGOLI	421	
LktB	QMTDTWOKQ	LASYVVSF	RVTVLATIG	QQGVOLIQ	TVMVNLWL	GAKLVISGD	LSIGOLI	412	
ApXIB	QMTTWOKQ	LASYVAGP	RVTVLATIG	QQGVOLIQ	TVMVNLWL	GAKLVISGD	LSIGOLI	411	
HlyB	QMTNIMDKQ	LAGYVAGP	RVTVLATIG	QQGVOLIQ	TVMVNLWL	GAKLVISGD	LSIGOLI	411	
MbxB	AFNMLAGQV	AAPVIRLAQ	LWQDPQQVC	ISVARLGDV	LSPTSTST	SLLTLPIN	GDITPEN	482	
LktB	AFNMLSGQV	IAPVIRLAQ	LWQDPQQVC	ISVTRLGDV	LSPTSTST	GRSLPPEIN	GDITPEN	473	
ApXIB	AFNMLSGQV	IAPVIRLAQ	LWQDPQQVC	ISVTRLGDV	LSPTSTST	GRSLPPEIN	GDITPEN	472	
HlyB	AFNMLAGQV	IAPVIRLAQ	LWQDPQQVC	ISVTRLGDV	LSPTSTST	GRSLPPEIN	GDITPEN	472	
MbxB	MDFRYKIDG	HLILQHLNL	QINAGEIG	IVGRSGSGK	STLTKLQR	LYFPENGR	MDGNOL	543	
LktB	IRFRYKIDG	HLILQHLNL	QINAGEIG	IVGRSGSGK	STLTKLQR	LYFPENGR	LIDGDL	534	
ApXIB	IRFRYKIDG	HLILQHLNL	QINAGEIG	IVGRSGSGK	STLTKLQR	LYFPENGR	LIDGDL	533	
HlyB	IRFRYKIDG	HLILQHLNL	QINAGEIG	IVGRSGSGK	STLTKLQR	LYFPENGR	LIDGDL	533	
MbxB	ALADPFWLR	ROGVVLQD	NVLLERSIR	DNIALSDPG	MSBFIHOA	ARSGABDP	IMELPEG	604	
LktB	ALADPFWLR	ROGVVLQD	NVLLERSIR	DNIALSDPG	MSBFIHOA	ARSGABDP	ISELREG	595	
ApXIB	ALADPFWLR	ROGVVLQD	NVLLERSIR	DNIALSDPG	MSBFIHOA	ARSGABDP	ISELREG	594	
HlyB	ALADPFWLR	ROGVVLQD	NVLLERSIR	DNIALSDPG	MSBFIHOA	ARSGABDP	ISELREG	594	
MbxB	YDTIVGEGQ	AGLSGGQRO	RIAIARALV	IMPILIPD	BATSALDYE	SEBAINQBM	QAICQGR	665	
LktB	YDTIVGEGQ	AGLSGGQRO	RIAIARALV	IMPILIPD	BATSALDYE	SEBAINQBM	QAICQGR	656	
ApXIB	YDTIVGEGQ	AGLSGGQRO	RIAIARALV	IMPILIPD	BATSALDYE	SEBAINQBM	QAICQGR	655	
HlyB	YDTIVGEGQ	AGLSGGQRO	RIAIARALV	IMPILIPD	BATSALDYE	SEBAINQBM	QAICQGR	655	
MbxB	TVIIAHRL	STVRMAHRI	IAMRGKIV	EQGSHBELL	QKQGYRY	LYDLQNG	717		
LktB	TVIIAHRL	STVRMAHRI	IAMRGKIV	EQGSHBELL	QKQGYRY	LYDLQNG	708		
ApXIB	TVIIAHRL	STVRMAHRI	IAMRGKIV	EQGSHBELL	QKQGYRY	LYDLQNG	707		
HlyB	TVIIAHRL	STVRMAHRI	IAMRGKIV	EQGSHBELL	QKQGYRY	LYDLQNG	707		

SEQIDNO:  
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SEQ ID NO: 13  
 SEQ ID NO: 14  
 SEQ ID NO: 20  
 SEQ ID NO: 21

# FIG. 10

DNASIS Translation Editor [11-00 C gene.dna]

1	ATGACGAAAAAGTTTGCAGAGCTAGGTTTAATTGCATGGCTTTGGTCTAACTCTGATATG	60
1	M T K K F A E L G L I A W L W S N S D M	20
61	CATAAACATTGGACGTTGTCTTTGTTTGGACCAATGTTATCCGGCAATTGAGACAGGT	120
21	H K H W T L S L F A T N V I P A I E T G	40
121	CAATATGTTATATTGAAAAGAGAAGATATGCCTGTAGCATATTGTAGTTGGGCTAAACTT	180
41	Q Y V I L K R E D M P V A Y C S W A K L	60
181	AGTTTAGAAAAACGAGGTTAAATATATTAACGATGTTACTTCTCTTAAGTTAGATGACTGG	240
61	S L E N E V K Y I N D V T S L K L D D W	80
241	CAGTCAGGTGACCGAAACTGGTTTATTGACTGGATTGCTCCATTTGGCGATAGTCTTACA	300
81	Q S G D R N W F I D W I A P F G D S L T	100
301	CTCACAAAACACATGAGAACGTTATTTTCAGATGAATTGTTTAGAGCGATTCTGTAGAT	360
101	L T K H M R T L F S D E L F R A I R V D	120
361	GGAAATTCATCGCATGGTAAGATATCTGAATTTTATGGAAAGTCTGTTGATTCAAAATTA	420
121	G N S S H G K I S E F Y G K S V D S K L	140
421	GCCTCAAGAATATTTGCACAATATCACGAAGATTTGACGAGCAAATTGTCAACTCAGAAT	480
141	A S R I F A Q Y H E D L T S K L S T Q N	160
481	AATTTTATTATATCTAAAGATAATTAA	507
161	N F I I S K D N *	169

SEQ ID NO: 31  
SEQ ID NO: 32

mbx C  
Mbx C

# FIG. 11

MbxC	- - - M T K K F A E	L G L I A W L W S N	S D E K H W T L S	L F A T N V I P A I	E T G Q Y	42
LktC	- - - M N Q S Y F N L	L G N I T W L W M N	S S L E K E W S C E	L L A R N V I P A I	E N E Q Y	43
ApXIC	M S K K I N G F E V	L G E V A W L W A S	S P L B R K W P L S	L L A I N V L P A I	E S N Q Y	45
HlyC	- M N R N N P L E V	L G R V S W L W A S	S P L B R N W P V S	L F A I N V L P A I	R A N Q Y	44

MbxC	V L K R D M P V	A Y C S W A K L S L	E N E V K Y I N D V	T S L K L D D W Q S	G D R N W	87
LktC	M L L I D N G I P I	A Y C S W A D L N L	E T E V K Y I K D V	N S L T P E W Q S	G D R R W	88
ApXIC	V L L K R D G F P I	A Y C S W A N L N L	E N E I K Y L D D V	A S L V A D D W T S	G D R R W	90
HlyC	A L L T R D N Y P V	A Y C S W A N L S L	E N E I K Y L N D V	T S L V A E D W T S	G D R W	89

MbxC	F I D W I A P F G D	S L T L T K H M R T	L F S D E L F R A I	R V D G N S S . H G	K I S E F	131
LktC	I I D W I A P F G H	S Q L L Y K K M C Q	K F P D M I V R S I	R F Y P K Q K E L G	K I A Y P	133
ApXIC	F I D W I A P F G D	S A A L Y K H M R D	N F P N E L F R A I	R V D P D S R . V G	K I S E F	134
HlyC	F I V W I A P F G D	N G A L Y K K M R K	K F P D E L F R A I	R V D P K T H . V G	K I S E F	133

MbxC	E G K S V D S K L A	S E I F A Q Y B E E	L T S K L S T Q N N	P I I S K D N -	168
LktC	K G G K D K K T A	K K R F D T Y O E E	L A T A L K N E F N	P I K K - - -	167
ApXIC	H G G K I D K K L A	S K I F Q Q Y H F E	L M S E L K N K Q N	P K F S L V N S	172
HlyC	H G G K I D R Q L A	N K I P K Q Y H E E	L I T E V K N R S D	P N F S L T G -	170

SEQ ID NO: 32  
 SEQ ID NO: 33  
 SEQ ID NO: 34  
 SEQ ID NO: 35



1321 CCAGGAATGAATGTTACTGCTGAAATTAAAACAGGTAAACGTCGTGTTTTGGATTATATA 1380  
441 P G M N V T A E K T G K R R V L D Y I 460  
1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTCGAGAACGCTAA 1428  
461 L S P L Q T K V D E S F R E R \* 476

SEQ ID NO: 36  
SEQ ID NO: 37

FIG. 12-2

1321 CCAGGAATGAATGTTACTGCTGAAATTAAAACAGGTAAACGTCGTGTTTTGGATTATATA

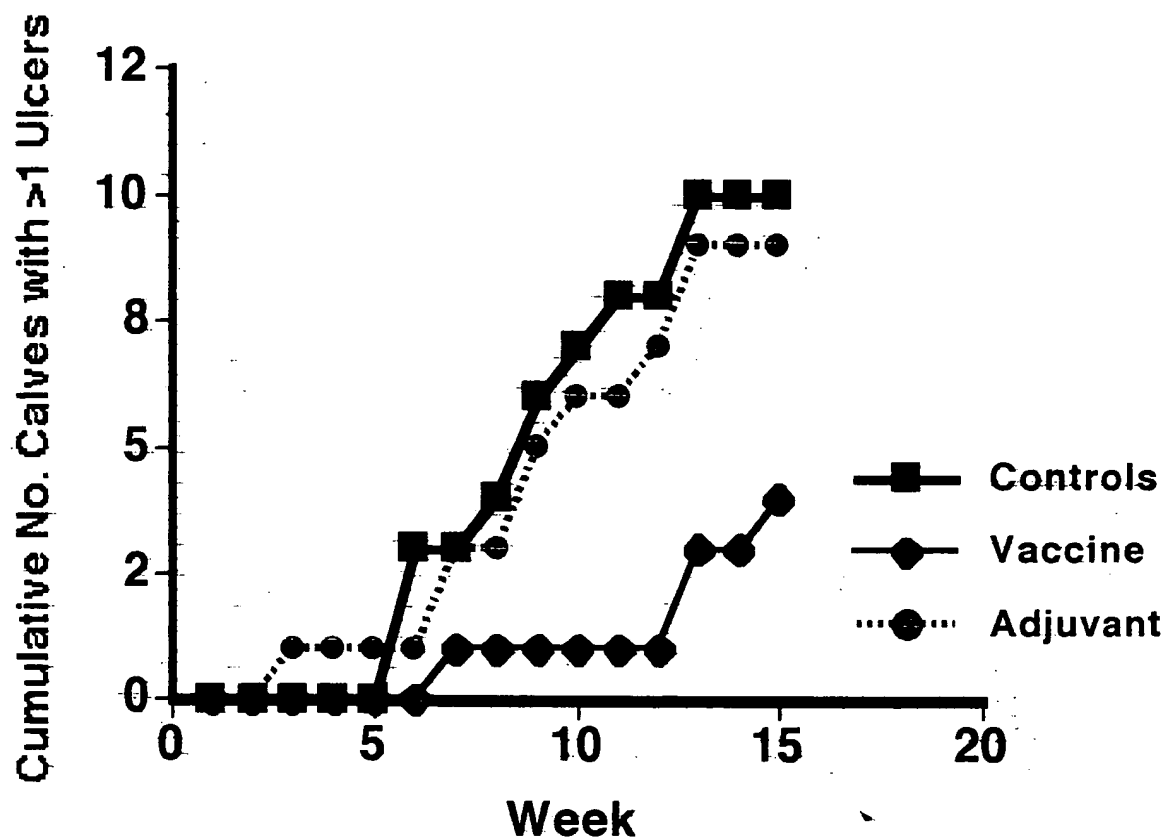
[illegible]

SEQ ID NO: 37  
SEQ ID NO: 38  
SEQ ID NO: 39  
SEQ ID NO: 40



F16.14

### Cumulative Number of Calves With Severe Ulcers



Number of calves with ulcers with clinical scores  $\geq +2$

FIG 15

# Number of calves affected each week

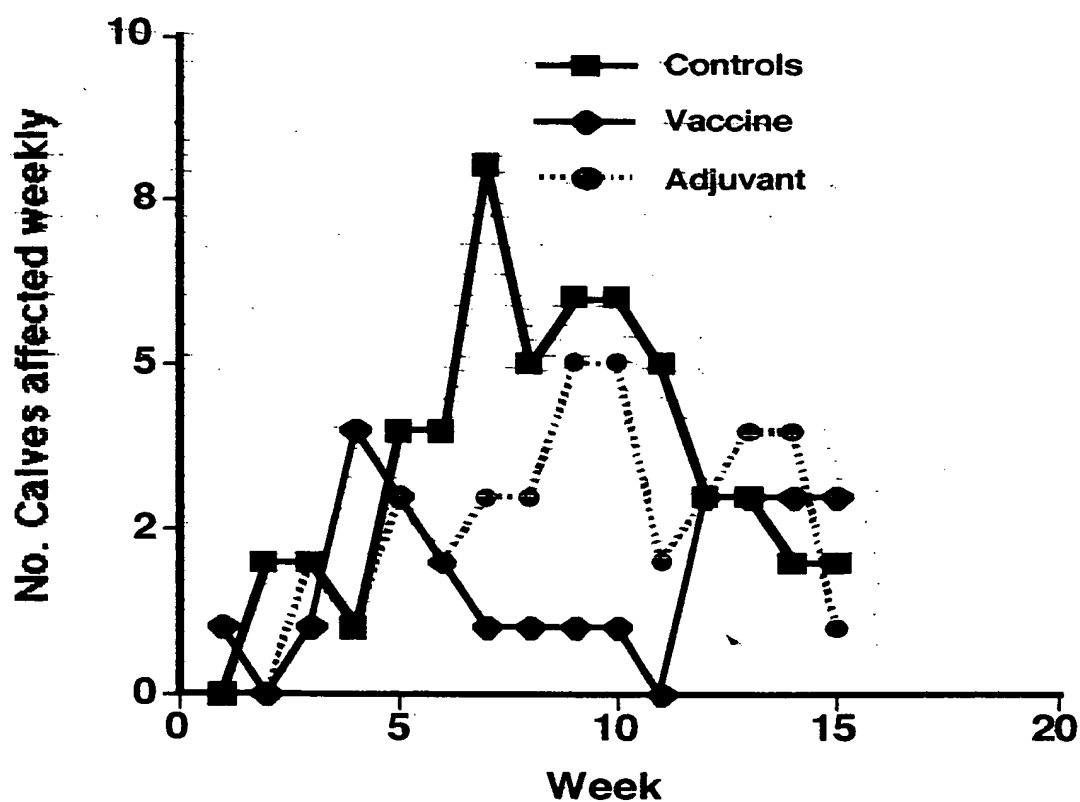
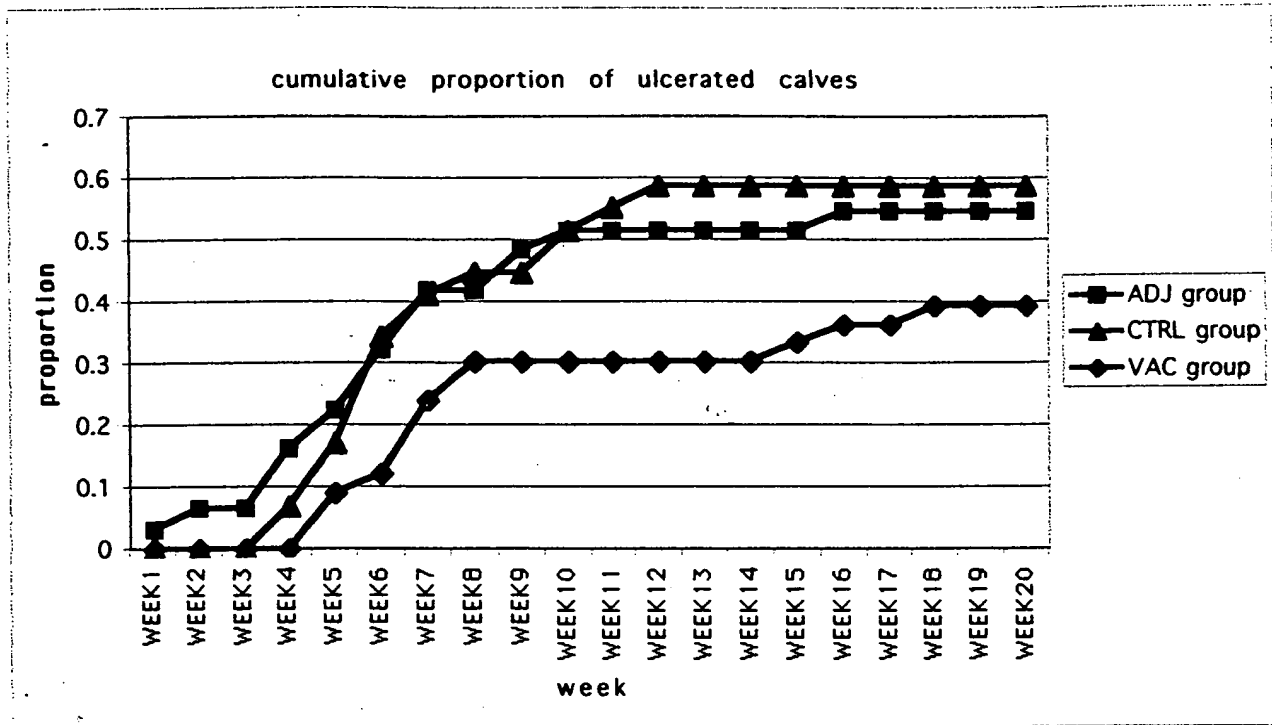


Figure 15  
Number of calves affected weekly in 1 group of vaccinated calves and in controls.

FIG. 16



Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').

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